

SEQUENCE LISTING

<110> Patience, Clive
Oldmixon, Beth
Ericsson, Thomas

<120> Molecular Sequence of Pig Endogenous Retrovirus Receptor and Methods of Use

<130> 329579-3

<150> US/60/285,103

<151> 2001-04-20

<160> 23

<170> PatentIn version 3.0

<210> 1

<211> 1959

<212> DNA

<213> Viral

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Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Ile Ile Asn Lys Leu Ile					
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 <212> DNA
 <213> Viral

<400> 3

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 Ser Pro Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp
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 Ser Gly Thr Gly Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu
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 Gly Thr Trp Trp Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
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 Gly Leu Asn Asp Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly
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 Phe Tyr Val Cys Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn
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<210> 9
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<213> Homo sapiens

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355 360 365
 Ser Ala Gly Val Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly
 370 375 380
 Val Phe Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly
 385 390 395 400
 Gly Arg Pro Ala Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser
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35 40 45
Ser Tyr Val Ser Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val
50 55 60
Val Thr Leu Trp Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro
65 70 75 80
Ile Arg Val Val Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala
85 90 95
Ser Leu Trp His His Val Ala Pro Val Ala Gly Gln Leu His Ser Val
100 105 110
Ala Phe Leu Ala Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser
115 120 125
Asn Val Thr Phe Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu
130 135 140
Arg Ser Phe Phe Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val
145 150 155 160
Leu Ala Leu Val Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro
165 170 175
Ile Asn Gly Thr Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro
180 185 190
Ala Ser Thr Phe Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala
195 200 205
Ala Ala Phe Gln Gly Leu Leu Leu Leu Pro Pro Pro Pro Ser Val
210 215 220
Pro Thr Gly Glu Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala
225 230 235 240
Glu Glu Glu Val Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln
245 250 255
Ala Ala Gly Thr Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu
260 265 270
Ser Ala Arg Ser Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala
275 280 285
Leu Thr Asn Gly Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro

290		295		300
Tyr Gly Arg Leu Ala	Tyr His Leu Ala Val	Val Leu Gly Ser Ala Ala		
305	310	315	320	
Asn Pro Leu Ala Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu				
	325	330	335	
Ala Gly Leu Gly Ser Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr				
	340	345	350	
Leu Met Ala Leu Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr				
	355	360	365	
Ser Ala Gly Val Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly				
	370	375	380	
Val Phe Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly				
385	390	395	400	
Gly Arg Pro Ala Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser				
	405	410	415	
Leu Leu Gly Ala Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val				
	420	425	430	
Phe His Ser Arg Lys Asp Cys Ala Asp Pro Cys Asp Ser				
	435	440	445	

<210> 13
 <211> 1473
 <212> DNA
 <213> Homo sapiens

<400> 13
 aaagcatctt tggacctacc tagggaagga cctgcctgtg acctttgccc tgtcctggag 60
 ggtccagctt tgggctgaat ggcagcacc acgctgggcc gtctggtgct gaccacctg 120
 ctggtggccc tttttggcat gggctcctgg gctgctgtga acgggatctg ggtggagctg 180
 cctgtggtgg taaaagacct tccagagggg tggagcctcc cctcatacct ctctgtggtt 240
 gtggcgctgg gaaacctggg tctgctggtg gtgacctgt ggaggcggct ggccccgggc 300
 aagggcgagc aggtcccat ccaggtggtg caggtgctga gtgtagtggg cacagccctg 360
 ctggcccctc tgtggcacca cgtggcccca gtggcagggc agctccactc tgtggccttc 420
 ctaactctgg ccttggtggt ggcaatggcc tgttgtaacct ctaatgtcac tttcctgccc 480
 ttcctgagcc acctgccacc tcctttctta cggcttttct tcctgggtca gggctcagt 540
 gccctactcc cctgtgtgct ggccttagtg caaggtgtgg gccgcctcga gtgcccacca 600
 gcgcccacca atggcacctc tgggcctccc ctgacttcc ctgagcgttt tcctgccagc 660
 accttcttct gggcactgac tgcccttctg gtcacttcag ctgccgcctt ccgggggtctc 720
 ctggttgctgt tgccatcagt accctctgta accacagggg gctcagggcc tgaacttcaa 780
 ctgggacccc caggagcaga ggaggaagag aaggaggaag aagaggcttt gccattgcag 840
 gagccaccga gccaggcagc aggcaccatc cctggcccag accctgaggc ccatcagctg 900
 ttctcagccc atggtgcctt cctgctgggc ctgatggcct tcaccagtgc cgtgaccaat 960
 ggcattgctg cttctgtgca gagcttttcc tgtttgccct atgggcgcct ggccctaccac 1020
 ctggctgtgg tgctgggcag tgccgccaac ccccttgccct gcttcctggc catgggcgtg 1080
 ctgtgcaggt ccctggcagg gctgggttgg ctttctctgc tgggcatgct ctttggggcc 1140
 tacctgatgg cactggcaat cctgagcccc tgcccacccc tgggtgggcac cactgcaggg 1200
 gtggtccttg tgggtgctgc gtgggtgctg tgtctgtgtg tgttctcata tgtgaaggtg 1260
 gctgcaagct ccctgctgca tgggtgggggt cggccggcat tgctggcagc tgggtgtggcc 1320

atccaagtgg gctccctgct tgggtgccggt gccatgttcc ctcccaccag catctaccac 1380
 gtgtttcaaa gcagaaagga ctgtgtagac ccctgtggcc cctgagcctg ggcaggtggg 1440
 gaccaactc caccacacct gtcttcacg tga 1473

<210> 14
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Ala Pro Thr Leu Gly Arg Leu Val Leu Thr His Leu Leu Val
 1 5 10 15
 Ala Leu Phe Gly Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val
 20 25 30
 Glu Leu Pro Val Val Val Lys Asp Leu Pro Glu Gly Trp Ser Leu Pro
 35 40 45
 Ser Tyr Leu Ser Val Val Val Ala Leu Gly Asn Leu Gly Leu Leu Val
 50 55 60
 Val Thr Leu Trp Arg Arg Leu Ala Pro Gly Lys Gly Glu Gln Val Pro
 65 70 75 80
 Ile Gln Val Val Gln Val Leu Ser Val Val Gly Thr Ala Leu Leu Ala
 85 90 95
 Pro Leu Trp His His Val Ala Pro Val Ala Gly Gln Leu His Ser Val
 100 105 110
 Ala Phe Leu Thr Leu Ala Leu Val Leu Ala Met Ala Cys Cys Thr Ser
 115 120 125
 Asn Val Thr Phe Leu Pro Phe Leu Ser His Leu Pro Pro Pro Phe Leu
 130 135 140
 Arg Ser Phe Phe Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val
 145 150 155 160
 Leu Ala Leu Val Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro
 165 170 175
 Thr Asn Gly Thr Ser Gly Pro Pro Leu Asp Phe Pro Glu Arg Phe Pro
 180 185 190
 Ala Ser Thr Phe Phe Trp Ala Leu Thr Ala Leu Leu Val Thr Ser Ala
 195 200 205
 Ala Ala Phe Arg Gly Leu Leu Leu Leu Leu Pro Ser Leu Pro Ser Val
 210 215 220
 Thr Thr Gly Gly Ser Gly Pro Glu Leu Gln Leu Gly Ser Pro Gly Ala
 225 230 235 240
 Glu Glu Glu Glu Lys Glu Glu Glu Glu Ala Leu Pro Leu Gln Glu Pro
 245 250 255

Pro Ser Gln Ala Ala Gly Thr Ile Pro Gly Pro Asp Pro Glu Ala His
260 265 270

Gln Leu Phe Ser Ala His Gly Ala Phe Leu Leu Gly Leu Met Ala Phe
275 280 285

Thr Ser Ala Val Thr Asn Gly Met Leu Pro Ser Val Gln Ser Phe Ser
290 295 300

Cys Leu Pro Tyr Gly Arg Leu Ala Tyr His Leu Ala Val Val Leu Gly
305 310 315 320

Ser Ala Ala Asn Pro Leu Ala Cys Phe Leu Ala Met Gly Val Leu Cys
325 330 335

Arg Ser Leu Ala Gly Leu Val Gly Leu Ser Leu Leu Gly Met Leu Phe
340 345 350

Gly Ala Tyr Leu Met Ala Leu Ala Ile Leu Ser Pro Cys Pro Pro Leu
355 360 365

Val Gly Thr Thr Ala Gly Val Val Leu Val Val Leu Ser Trp Val Leu
370 375 380

Cys Leu Cys Val Phe Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu
385 390 395 400

His Gly Gly Gly Arg Pro Ala Leu Leu Ala Ala Gly Val Ala Ile Gln
405 410 415

Val Gly Ser Leu Leu Gly Ala Gly Ala Met Phe Pro Pro Thr Ser Ile
420 425 430

Tyr His Val Phe Gln Ser Arg Lys Asp Cys Val Asp Pro Cys Gly Pro
435 440 445

<210> 15
<211> 1347
<212> DNA
<213> Baboon

<400> 15
atggcagcac ccacgctggg ccatctggtg ctgaccacac tgctggtggc ctttctcggc 60
atgggctcct gggctgctgt caacggcatc tgggtggagc tacctgtggt ggtaaaacac 120
cttccagagg gttggagcct cccctcatac ctctctgtgg ttgtggcact gggaaacctg 180
ggctctgctgg tggtagctct gtggaggcgg ctggccccgg gcaagggcga gcgggtcccc 240
atccaggtgg tacaggtgct gagtgtagtg ggcacagccc tgctggcccc tctgtggcac 300
cacgtggccc cagtggcagg gcaactccac tccgtggcct tcctaactac ggccttagtg 360
ttggcactgg cctgctgtac ctctaattgc actttcctgc ccttcctgag ccacctgcca 420
cctcctttct tacggtcttt cttcctgggt cagggtctca gtgccctgct cccctgtgtg 480
ctagccctag tgcagggtgt aggcgcctc gagtgtctgc cagcgccac caatggcacc 540
tcagggcctc ccctcaactt cctgagcgt tttcctgcca gcaccttcta ctgggactg 600
actgcccttc tggtagcttc ggctgccgcc ttccagggtc tcctgttgct gttgccatca 660
ctaccatctg taaccacagg gggcgaggg cctgaacttc cactgggatc cccaggagca 720
gaggaggaag agaaggagga agaagaggct ttgccattgc aggagccacc aagccaggca 780
gcaggcacca tccttgggcc agaccctgag gcccatcagc tgttctcagc ccatggtgcc 840

ttcctgctgg	gcctgctggc	catcaccagt	gccctgacca	atggcgtgct	gcctgccgtg	900
cagagccttt	cctgtttgcc	ctatgggcgc	ttggcctacc	acctggctgt	ggtgctgggc	960
agtgcgcgca	accccttgcc	ctgcttcctg	gccatgggcg	tgctgtgcag	gtccctggca	1020
gggctgggtg	gtctttctct	gctgggcatg	ctctttgggg	cctacctgat	ggtactggca	1080
atcctgagcc	cctgcccacc	cctgggtggc	accaccgcag	gggtggctct	tgtggtactg	1140
tcgtgggtgc	tgtgtctttg	tgtgttctca	tacgtgaagg	tggtgcaag	ctccctgctg	1200
catgggtggg	gtcggccggc	attgctggcg	gctgggtgtg	ccatccagat	gggctccctg	1260
cttgggtgcc	gcaccatgtt	ccctcctacc	agcatctacc	acgtgtttca	aagcagaaag	1320
gactgtgtag	acccctgtgg	cccctga				1347

<210> 16
 <211> 448
 <212> PRT
 <213> Baboon

<400> 16

Met	Ala	Ala	Pro	Thr	Leu	Gly	His	Leu	Val	Leu	Thr	His	Leu	Leu	Val	1	5	10	15
Ala	Leu	Leu	Gly	Met	Gly	Ser	Trp	Ala	Ala	Val	Asn	Gly	Ile	Trp	Val	20	25	30	
Glu	Leu	Pro	Val	Val	Val	Lys	His	Leu	Pro	Glu	Gly	Trp	Ser	Leu	Pro	35	40	45	
Ser	Tyr	Leu	Ser	Val	Val	Val	Ala	Leu	Gly	Asn	Leu	Gly	Leu	Leu	Val	50	55	60	
Val	Thr	Leu	Trp	Arg	Arg	Leu	Ala	Pro	Gly	Lys	Gly	Glu	Arg	Val	Pro	65	70	75	80
Ile	Gln	Val	Val	Gln	Val	Leu	Ser	Val	Val	Gly	Thr	Ala	Leu	Leu	Ala	85	90	95	
Pro	Leu	Trp	His	His	Val	Ala	Pro	Val	Ala	Gly	Gln	Leu	His	Ser	Val	100	105	110	
Ala	Phe	Leu	Thr	Leu	Ala	Leu	Val	Leu	Ala	Leu	Ala	Cys	Cys	Thr	Ser	115	120	125	
Asn	Val	Thr	Phe	Leu	Pro	Phe	Leu	Ser	His	Leu	Pro	Pro	Pro	Phe	Leu	130	135	140	
Arg	Ser	Phe	Phe	Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Leu	Pro	Cys	Val	145	150	155	160
Leu	Ala	Leu	Val	Gln	Gly	Val	Gly	Arg	Leu	Glu	Cys	Ser	Pro	Ala	Pro	165	170	175	
Thr	Asn	Gly	Thr	Ser	Gly	Pro	Pro	Leu	Asn	Phe	Pro	Glu	Arg	Phe	Pro	180	185	190	
Ala	Ser	Thr	Phe	Tyr	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Thr	Ser	Ala	195	200	205	
Ala	Ala	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Leu	Pro	Ser	Val	210	215	220	

Thr Thr Gly Gly Ala Gly Pro Glu Leu Pro Leu Gly Ser Pro Gly Ala
 225 230 235 240
 Glu Glu Glu Glu Lys Glu Glu Glu Glu Ala Leu Pro Leu Gln Glu Pro
 245 250 255
 Pro Ser Gln Ala Ala Gly Thr Ile Pro Gly Pro Asp Pro Glu Ala His
 260 265 270
 Gln Leu Phe Ser Ala His Gly Ala Phe Leu Leu Gly Leu Leu Ala Ile
 275 280 285
 Thr Ser Ala Leu Thr Asn Gly Val Leu Pro Ala Val Gln Ser Phe Ser
 290 295 300
 Cys Leu Pro Tyr Gly Arg Leu Ala Tyr His Leu Ala Val Val Leu Gly
 305 310 315 320
 Ser Ala Ala Asn Pro Leu Ala Cys Phe Leu Ala Met Gly Val Leu Cys
 325 330 335
 Arg Ser Leu Ala Gly Leu Val Gly Leu Ser Leu Leu Gly Met Leu Phe
 340 345 350
 Gly Ala Tyr Leu Met Val Leu Ala Ile Leu Ser Pro Cys Pro Pro Leu
 355 360 365
 Val Gly Thr Thr Ala Gly Val Val Leu Val Val Leu Ser Trp Val Leu
 370 375 380
 Cys Leu Cys Val Phe Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu
 385 390 395 400
 His Gly Gly Gly Arg Pro Ala Leu Leu Ala Ala Gly Val Ala Ile Gln
 405 410 415
 Met Gly Ser Leu Leu Gly Ala Gly Thr Met Phe Pro Pro Thr Ser Ile
 420 425 430
 Tyr His Val Phe Gln Ser Arg Lys Asp Cys Val Asp Pro Cys Gly Pro
 435 440 445

<210> 17
 <211> 445
 <212> PRT
 <213> Artificial

<220>
 <223> Consensus sequence of SEQ ID NO: 12, 14 and 16.

<400> 17
 Met Ala Ala Pro Thr Leu Gly Arg Leu Val Leu Thr His Leu Leu Val
 1 5 10 15
 Ala Leu Phe Gly Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val
 20 25 30

Glu	Leu	Pro	Val	Val	Val	Lys	Leu	Pro	Glu	Gly	Trp	Ser	Leu	Pro	Ser	35	40	45
Tyr	Leu	Ser	Val	Val	Val	Ala	Leu	Gly	Asn	Leu	Gly	Leu	Leu	Val	Val	50	55	60
Thr	Leu	Trp	Arg	Arg	Leu	Ala	Pro	Gly	Lys	Gly	Glu	Gln	Val	Pro	Ile	65	70	75
Gln	Val	Val	Gln	Val	Leu	Ser	Val	Val	Gly	Thr	Ala	Leu	Leu	Ala	Pro	85	90	95
Leu	Trp	His	His	Val	Ala	Pro	Val	Ala	Gly	Gln	Leu	His	Ser	Val	Ala	100	105	110
Phe	Leu	Thr	Leu	Ala	Leu	Val	Leu	Ala	Leu	Ala	Cys	Cys	Thr	Ser	Asn	115	120	125
Val	Thr	Phe	Leu	Pro	Phe	Leu	Ser	His	Leu	Pro	Pro	Pro	Phe	Leu	Arg	130	135	140
Ser	Phe	Phe	Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Leu	Pro	Cys	Val	Leu	145	150	155
Ala	Leu	Val	Gln	Gly	Val	Gly	Arg	Leu	Glu	Cys	Pro	Pro	Ala	Pro	Thr	165	170	175
Asn	Gly	Thr	Ser	Gly	Pro	Pro	Leu	Asp	Phe	Pro	Glu	Arg	Phe	Pro	Ala	180	185	190
Ser	Thr	Phe	Phe	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Thr	Ser	Ala	Ala	195	200	205
Ala	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Leu	Pro	Ser	Val	Thr	210	215	220
Thr	Gly	Gly	Gly	Pro	Glu	Leu	Gln	Leu	Gly	Ser	Pro	Gly	Ala	Glu	Glu	225	230	235
Glu	Glu	Lys	Glu	Glu	Glu	Glu	Ala	Leu	Pro	Leu	Gln	Glu	Pro	Pro	Ser	245	250	255
Gln	Ala	Ala	Gly	Thr	Ile	Pro	Gly	Pro	Asp	Pro	Glu	Ala	His	Gln	Leu	260	265	270
Phe	Ser	Ala	His	Gly	Ala	Phe	Leu	Leu	Gly	Leu	Leu	Ala	Thr	Ser	Ala	275	280	285
Leu	Thr	Asn	Gly	Val	Leu	Pro	Ala	Val	Gln	Ser	Phe	Ser	Cys	Leu	Pro	290	295	300
Tyr	Gly	Arg	Leu	Ala	Tyr	His	Leu	Ala	Val	Val	Leu	Gly	Ser	Ala	Ala	305	310	315
Asn	Pro	Leu	Ala	Cys	Phe	Leu	Ala	Met	Gly	Val	Leu	Cys	Arg	Ser	Leu	325	330	335

Ala Gly Leu Val Gly Leu Ser Leu Leu Gly Met Leu Phe Gly Ala Tyr
340 345 350

Leu Met Ala Leu Ala Ile Leu Ser Pro Cys Pro Pro Leu Val Gly Thr
355 360 365

Thr Ala Gly Val Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Cys
370 375 380

Val Phe Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly
385 390 395 400

Gly Arg Pro Ala Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser
405 410 415

Leu Leu Gly Ala Gly Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val
420 425 430

Phe Gln Ser Arg Lys Asp Cys Val Asp Pro Cys Gly Pro
435 440 445

<210> 18

<211> 19

<212> DNA

<213> Artificial

<220>

<223> PCR Primer Oligonucleotide

<400> 18

cccagtggca ggacagttg

19

<210> 19

<211> 16

<212> DNA

<213> Artificial

<220>

<223> PCR Primer Oligonucleotide

<400> 19

tcagcgcgtt ggtggc

16

<210> 20

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR Primer Oligonucleotide

<400> 20

gtkaccttyg cykwccttg

20

<210> 21
<211> 19
<212> DNA
<213> Artificial

<220>
<223> PCR Primer Oligonucleotide

<400> 21
ggagykgggt cccacctg

19

<210> 22
<211> 17
<212> DNA
<213> Artificial

<220>
<223> PCR Primer Oligonucleotide

<400> 22
aatggcagca ccymcgc

17

<210> 23
<211> 18
<212> DNA
<213> Artificial

<220>
<223> PCR Primer Oligonucleotide

<400> 23
tcaggggccca caggggtc

18